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10/054,611	01/18/2002	Thomas R. Cech	015389-002970US	9312

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TOWNSEND AND TOWNSEND AND CREW LLP
8TH FLOOR
TWO EMBARCADERO CENTER
SAN FRANCISCO, CA 94111

EXAMINER	
WALICKA, MALGORZATA A	
ART UNIT	**PAPER NUMBER**
1652	5

DATE MAILED: 01/05/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/054,611	CECH ET AL.	
	Examiner	Art Unit	
	Malgorzata A. Walicka	1652	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE ____ MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☐ Responsive to communication(s) filed on _____.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-34* is/are pending in the application.

4a) Of the above claim(s) *23-34* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☐ Claim(s) *1-22* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☒ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. §§ 119 and 120

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

13)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application) since a specific reference was included in the first sentence of the specification or in an Application Data Sheet. 37 CFR 1.78.

a) ☐ The translation of the foreign language provisional application has been received.

14)☒ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121 since a specific reference was included in the first sentence of the specification or in an Application Data Sheet. 37 CFR 1.78.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☒ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449) Paper No(s) *1*.
4) ☐ Interview Summary (PTO-413) Paper No(s). _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: *sequence alignment*.

The application, filed January 18, 2002 is acknowledged. Claims 1-34 are pending in the application. Claims 1-22 are the subject of this Office Action; claims 23-34 are withdrawn from consideration by examiner as directed to the non-elected invention.

DETAILED ACTION

1. Election/Restriction

Restriction to one of the following inventions is required under 35 U.S.C. 121:

I. Claims 1-22, drawn to a method of identifying a nucleic acid in a sample classified in class 435, subclass 6.

II. Claim 23-26, drawn to a combination of primers for PCR amplification, classified in class 536, subclass 24.3

III. Claim 27 drawn to a PCR product that hybridizes to the sequence of SEQ ID NO: 224, classified in class 536, subclass 24.5.

IV. Claim 28-34, and 14, drawn to a hybridization complex comprising human telomerase reverse transcriptase (hTRT), classified in class 536, subclass 23.1.

Inventions of Groups I and II-IV comprise a method, different chemical compositions (Group II and IV) and compound (Group III), having different structure and function. The compositions and the compound are not disclosed as capable of use together. The compositions of Groups II and IV and the compound of Group III cannot

be used in the method of Group I. Thus, inventions I-IV are unrelated. (MPEP § 806.04, MPEP § 808.01).

Inventions of Group I-IV are distinct for the reasons given above and have acquired a separate status in the art. Because of their recognized divergent subject matter and/or different classification, restriction for examination purposes as indicated is proper.

Applicant is reminded that upon the cancellation of claims to a non-elected invention, the inventorship must be amended in compliance with 37 CFR 1.48(b) if one or more of the currently named inventors is no longer an inventor of at least one claim remaining in the application. Any amendment of inventorship must be accompanied by a petition under 37 CFR 1.48(b) and by the fee required under 37 CFR 1.17(i).

During a telephone conversation with Applicants' representative Michael Schiff, on December 10, 2003, a provisional election was made, without traverse, to prosecute the invention of Group I, claims 1-22. Affirmation of this election must be made by Applicant in replying to this Office Action.

Claims 23-34 are withdrawn from further consideration by the examiner as being drawn to a non-elected invention; see 37 CFR 1.142(b).

2. Objections

2.1. Priority

The examiner acknowledges the claim to priority, however, Applicants have not been granted priority to the US application No. 08/724,643 for the instant claims,

because said application does not contain the subject matter claimed in the instant application. Specifically, the disclosure of the US application No. 08/724,643 is not related to the human telomerase reverse transcriptase.

In addition, the examiner acknowledges the claim to priority to US Application NO. 08/844,419 and 08/846017. Applicants, however, have not been granted priority to these US applications for the instant claims, because neither one of these applications discloses the polynucleotide sequence that is identified as SEQ ID NO: 224 in the instant application.

2.2. Specification

Page 16 and 82 contain empty space after the "ATCC accession #".

Page 11, second line from the bottom, "the nucleotide of SEQ ID NO: 100" should be replaced with "the polynucleotide of SEQ ID No: 100". In the last line on page 11 and further on page 12 "with the nucleotide under", and "between the nucleic acid and the nucleotide" should be replaced with "with the polynucleotide under", and "between the nucleic acid and the polynucleotide".

The specification has not been checked to the extent necessary to determine the presence of all possible minor errors. Applicant's cooperation is requested in correcting any errors in the specification of which applicant may become aware.

2.3. Drawings

Formal drawings will be required when the application is allowed; see the attached form PTO 948.

2.4. Claims

Claim 13 and 14 objected to because of the following informalities. The claims use the phrase "primer amplifies", which is a laboratory jargon. A primer primes. Appropriate correction is required.

The term "portion of " in claims 1 and 14 should be replaced by "a fragment of".

3. Rejections

3.1. 35 USC, section 112, second paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter, which the applicant regards as his invention.

Claims 1 and 2 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention

Claim 1 and 2 are rejected because the claims are directed to the methods of identifying/detecting a nucleic acid comprising step a) in which a probe "hybridizes to the nucleic acid". The phrase "hybridizes to the nucleic acid" renders the claim

indefinite. There are many sets of hybridization conditions in the prior art that are used for identifying DNA molecules by hybridization. Applicants exemplify hybridization conditions on page 20, but there is nothing to suggest that other conditions are excluded from the scope of the claim. Including the hybridization conditions in the claims would overcome this rejection.

Claims 3-12 are included in the rejection as depending from claim 2, because they do not correct the language of the base claim.

3.2. 35 USC, section 112, first paragraph

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

3.2.1. Lack of written description

Claims 1-22 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter, which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Claim 1 is directed to a large and variable genus of methods of identifying the nucleic acid as encoding at least a fragment of human telomerase reverse transcriptase, said methods using a genus of polynucleotide probes comprising a sequence identical or complementary to at least 10 consecutive nucleotides of SEQ ID NO: 224.

The methods use large and variable genus of polynucleotides. Their structures are not sufficiently disclosed in the application. The specification discloses many species of the genus of these probes, such as SEQ ID NO: 62, 100 or primers of SEQ ID Nos: 87-99. This is, however, insufficient to put one of skill in the art in possession of the attributes and features of all species within the genus of probes to be used. The disclosure teaches the probes that consists of fragments of SEQ ID NO: 224, the scope of the claim, however, is much broader and includes probes, which due to abundance of nucleotide not comprised in SEQ ID NO: 224 will not hybridize to any portion of human telomerase reverse transcriptase.

Given the lack of structural characteristics of additional representative species as encompassed by the claim, Applicants have failed to sufficiently describe the claimed invention in such full, clear, concise and exact terms that a skilled artisan would recognize Applicants were in possession of the claimed invention when the application was filed.

Claims 2-12 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described

in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are directed to a method of detecting a nucleic acid in a sample, comprising:

a) combining the sample with a polynucleotide probe such that the probe hybridizes to a nucleic acid comprising at least 100 consecutive nucleotides contained in SEQ ID NO: 224 if present in the sample ; and

b) detecting any hybrid formed as a result of a);

wherein the polynucleotide probe comprises a sequence identical or complementary to at least 25 consecutive nucleotides contained in SEQ ID NO:224.

The claims are directed to a large and variable genus of methods of detecting a nucleic acid said methods using a genus of polynucleotide probes comprising a sequence identical or complementary to at least 25 consecutive nucleotides of SEQ ID NO: 224 and hybridize to a nucleic acid comprising at least 100 consecutive nucleotides contained in SEQ ID NO: 224 if present in the sample.

The structures of the probes are not sufficiently disclosed in the application. The specification discloses many species of the genus of these probes, such as SEQ ID NO: 62, 100 or primers of SEQ ID Nos: 87-99. This is, however, insufficient to put one of

skill in the art in possession of the attributes and features of all species within the genus of probes to be used. The disclosure teaches the probes that consists of fragments of SEQ ID NO: 224, the scope of the claim, however, is much broader and includes probes, which due to abundance of nucleotide not comprised in SEQ ID NO: 224 will not hybridize to any portion of human telomerase reverse transcriptase.

Given the lack of structural characteristics of additional representative species as encompassed by the claim, Applicants have failed to sufficiently describe the claimed invention in such full, clear, concise and exact terms that a skilled artisan would recognize Applicants were in possession of the claimed invention when the application was filed.

Claims 14-22 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claim 14 is directed to a large and variable genus of methods of detecting a nucleic acid encoding at least a fragment of human telomerase using a genus of primers that initiate the amplification of at least a fragment of human telomerase and comprise a sequence identical or complementary to at least 15 consecutive nucleotides contained in SEQ ID NO: 224.

The structures of primers as recited by the claim are not sufficiently disclosed in the application. The specification teaches only probes that are fragments of SEQ ID

NO: 224, for example, primers of SEQ ID NOs: 87-99. The specification fails to teach any primer that comprises at least 15 nucleotides of SEQ ID NO: 224 and any number of nucleotides whose sequence is not that characteristic for a fragment of SEQ ID NO: 224. Thus, the disclosure is insufficient to put one of skill in the art in possession of the structural features of all species within the genus of probes to be used in the claimed genus of methods, because the polynucleotide as claimed by claim 14 may have any structure. Given the lack of structural characteristics of additional representative species as encompassed by the claim, Applicants have failed to sufficiently describe the claimed invention in such full, clear, concise and exact terms that a skilled artisan would recognize Applicants were in possession of the claimed invention when the application was filed.

Claims 15-22 are included into this rejection, because they do not correct the language of the claim from which they depend.

Claim 13 is rejected as directed to a large and variable genus of methods of identifying the nucleic acid as encoding at least a fraction of human telomerase reverse transcriptase, said methods using a genera of polynucleotide primers **containing** a sequence identical or complementary to at least 10 consecutive nucleotides of SEQ ID NO: 224.

The methods use large and variable genus of primers. Their structures are not sufficiently disclosed in the application. The specification discloses several species of the genus, e.g. primers of SEQ ID Nos: 87-99. This is, however, insufficient to put one

of skill in the art in possession of the attributes and features of all species within the genus of primers to be used as claimed. The disclosure teaches the primers that consists of fragments of SEQ ID NO: 224, the scope of the claim, however, is much broader and includes primers, which due to abundance of nucleotide not comprised in SEQ ID NO: 224 will not hybridize to any portion of human telomerase reverse transcriptase and will instead initiate amplification of DNA molecules that are not of interest.

Given the lack of structural characteristics of additional representative species as encompassed by the claim, Applicants have failed to sufficiently describe the claimed invention in such full, clear, concise and exact terms that a skilled artisan would recognize Applicants were in possession of the claimed invention when the application was filed.

2.2.2. Scope of enablement

Claim 1-12 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for the methods of using of probes consisting of the at least 10 consecutive nucleotides of SEQ ID NO: 224, does not reasonably provide enablement for use of the probes which

a) comprise at least 10 consecutive nucleotides of SEQ ID NO: 224,

b) comprise at least 25 consecutive nucleotides of SEQ ID NO: 224 and hybridize to a nucleic acid comprising at least 100 consecutive nucleotides contained in SEQ ID NO: 224.

The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims.

The claims are broader than the enablement provided by the disclosure with regard to the extremely large number of probes enumerated under a) and b) whose structure is not disclosed by Applicants; see the above rejection for lack of written description.

The scope of the claims must bear a reasonable correlation with the scope of enablement (In re Fisher, 166 USPQ 19 24 (CCPA 1970)). Otherwise, undue experimentation is necessary to make the claimed invention. Factors to be considered in determining whether undue experimentation is required, are summarized *In re* Wands [858 F.2d 731, 8 USPQ 2nd 1400 (Fed. Cir. 1988)]. The Wands factors are: (a) the nature of the invention, (b) the breadth of the claim, (c) the state of the prior art, (d) the relative skill of those in the art, (e) the predictability of the art, (f) the presence or absence of working example, (g) the amount of direction or guidance presented, (h) the quantity of experimentation necessary.

The nature and breath of the claimed invention encompasses any method of identifying or detecting a nucleic acid in a sample by hybridization, wherein the method uses the probes which

a) comprise at least 10 consecutive nucleotides of SEQ ID NO: 224,

b) comprise at least 25 consecutive nucleotides of SEQ ID NO: 224 and hybridize to a nucleic acid comprising at least 100 consecutive nucleotides contained in SEQ ID NO: 224.

While methods of detecting and identifying nucleic acid molecules using specific probes are well developed and skills of the artisans high the construction and selection of probes recited by claim 1-12 requires undue experimentation.

Claim 1 uses probes that contain at least 10 consecutive nucleotides of SEQ ID NO: 224 and any number of other nucleotide and hybridizes to the human telomerase or the fragment thereof. The structure of probes as recited by the claim encompasses a large and variable genus of polynucleotides most of which will not hybridize to the human telomerase in the sample but to other DNA molecules present in the sample. Thus, lack of the proper structural characteristics of the probes makes the probability of success in obtaining the claimed invention very low. Examiner concludes absent teaching the structure of probes undue experimentation is imposed on an artisan.

Similarly, regarding claims 2-12, a skilled artisan is required to construct a large and variable genus of probes that comprise any at least 25 consecutive nucleotides of SEQ ID NO: 224, than to construct a large and variable genus of nucleic acid molecules comprising any at least 100 consecutive nucleotides contained in SEQ ID NO: 224 and subsequently screen the first genus against the second to select the probes that comprise at least 25 consecutive nucleotides of SEQ ID NO: 224 and hybridize to a nucleic acid comprising at least 100 consecutive nucleotides contained in SEQ ID NO:224.

While enablement is not precluded by the necessity for routine screening, if a large amount of screening is required, the specification must provide a reasonable amount of guidance with respect to the direction in which the experimentation should proceed so that the probability of success in obtaining the claimed invention were high. The specification fails to provide such guidance because the several species of probes disclosed are limited to the fragments of SEQ ID NO: 224 and do not encompass species with major structural variations form the fragments, which remain encompassed within the scope of the rejected claims.

Thus to make and use the claimed invention requires undue experimentation.

3.3. 35 USC section 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

Claim 1 and 13 are rejected under 35 U.S.C. 103(a) as being unpatentable over Adams et al. homo sapiens cDNA sequence AA311750 (Initial assessment of human gene diversity and expression patterns based on 83 million nucleotides of cDNA sequence, Nature 377 (6547 Suppl), 3-174, 1995) in the view of common knowledge in the field of molecular biology.

The claims are directed to a method of identifying a nucleic acid in a sample, comprising:

a) combining the sample with a polynucleotide probe/primer comprising a sequence identical or complementary to at least 10 consecutive nucleotides contained in SEQ ID NO: 224, such that the probe hybridizes to the nucleic acid or the primer initiates amplification of the nucleic acid;

b) detecting any hybrid/amplification formed as a result of a); and

c) identifying the nucleic acid as encoding at least a fragment of human telomerase reverse transcriptase (h TRT) if the hybrid/amplification is detected.

Adams and al. teach Homo sapiens cDNA 5' sequence identified as locus AA311750. This EST sequence is 258 nucleotides long, and exhibits 97.7% homology with the fragment of SEQ ID NO: 224 which consists of nucleotides 2649-2906. AA311750 comprises 164 nucleotide long, 20 nucleotide long, and 64 nucleotide long consecutive fragments of SEQ ID NO: 224; see sequence alignment.

Adams et al. do not teach the use of 164, 64 and 20 nucleotide long fragments of AA311750 as probes/primers in hybridization/amplifying any nucleic acid in the sample. However, one skilled in the art knows that EST sequences are created to be used for detecting a presence of the sequences that are homologous to them.

It would have been obvious to one having ordinary skill in the art at the time of invention to use in step a) the AA311750 a sequence fragments and if any hybrids/amplification are detected in step b) to identify in step c) by a routine cloning

procedures, a bigger fragment or full length DNA comprising fragments of AA311750 such as a human telomerase reverse transcriptase or its fragment. The motivation is to use in identifying the telomerase reverse transcriptase the human EST molecules, because one of the purposes of the Genome Project is to produce the EST molecules that are subsequently used for finding the full-length genes. Thus, the claimed invention was within the ordinary skill in the art to make and use at the time it was made and was as a whole, *prima facie* obvious.

In addition, the rejection of claims 1 and 13 under 35 USC section 103 can be made using as the prior art cDNA sequence AA281296 disclosed by Straussberg; see the encloses NCBI Sequence Viewer printout. As indicted in the enclosed sequence alignment, the sequence covers nucleotides 1679-2067 of SEQ ID NO: 224. The sequence was entered to NBCI data base in April 1997.

Claims 2-12 are rejected under 35 U.S.C. 103(a) as being unpatentable over Adams et al. homo sapiens cDNA sequence AA311750 (Initial assessment of human gene diversity and expression patterns based on 83 million nucleotides of cDNA sequence, Nature 377 (6547 Suppl), 3-174, 1995) in the view of common knowledge in the field of molecular biology.

The claims are directed to a method of detecting a nucleic acid in a sample, comprising:

a) combining the sample with a polynucleotide probe such that the probe hybridizes to a nucleic acid comprising at least 100 consecutive nucleotides contained in SEQ ID NO: 224 if present in the sample; and

b) detecting any hybrid formed as a result of a);

wherein the polynucleotide probe comprises a sequence identical or complementary to at least 25 consecutive nucleotides contained in SEQ ID NO: 224.

Adams and al. teach Homo sapiens cDNA 5' sequence identified as locus AA311750. This EST sequence is 258 nucleotides long, and exhibits 97.7% homology with the fragment of SEQ ID NO: 224 which consists of nucleotides 2649-2906. AA311750 comprises 164 nucleotide long, 20 nucleotide long, and 64 nucleotide long consecutive fragments of SEQ ID NO: 224; see sequence alignment.

Adams et al. do not teach the use of 164 and 64 nucleotide long fragments as probes in detecting any nucleic acid in the sample. However, one skilled in the art knows that EST sequences are created to be used for detecting a presence of the sequences that are homologous to them.

It would have been obvious to one having ordinary skill in the art at the time of invention to use for detecting of a DNA the AA311750 sequence and knowing that the probe has to hybridizes to a nucleic acid comprising at least 100 consecutive nucleotides contained in SEQ ID NO: 224, to have fragments of AA311750 and use them for detecting a nucleic acid in a sample. Both longer fragments of AA311750 would hybridize to at least 100 consecutive nucleotides contained in SEQ ID NO: 224 if present in the sample. The motivation is to use in detecting hybridization assay a

polynucleotide that is identical to a fragment of the polynucleotide to be detected, because using such a probe gives 100% success in detecting said DNA molecule.

Thus, the claimed invention was within the ordinary skill in the art to make and use at the time it was made and was as a whole, *prima facie* obvious.

In addition, claims 2-9, 12 are rejected under 35 U.S.C. 103(a) as being unpatentable over Straussberg who discloses homo sapiens cDNA sequence AA281296, see the encloses NCBI Sequence Viewer printout. As indicted in the enclosed sequence alignment, the sequence covers nucleotides 1679-2067 of SEQ ID NO: 224. The sequence was entered to NBCI data base in April 1997.

The claims are directed to a method of detecting a nucleic acid in a sample, comprising:

a) combining the sample with a polynucleotide probe such that the probe hybridizes to a nucleic acid comprising at least 100 consecutive nucleotides contained in SEQ ID NO: 224 if present in the sample; and

b) detecting any hybrid formed as a result of a);

wherein the polynucleotide probe comprises a sequence identical or complementary to at least 25 consecutive nucleotides contained in SEQ ID NO: 224.

One skilled in the art knows that EST sequences are created to be used for detecting specific DNA molecules in a sample, namely such that hybridize to them. It would have been obvious, therefore, to one having ordinary skill in the art at the time of invention to use cDNA sequence AA281296 for detecting of a DNA sequence knowing

that the probe has to hybridizes to a nucleic acid comprising at least 100 consecutive nucleotides contained in SEQ ID NO: 224

The motivation would be to use in detecting hybridization assay a polynucleotide that is identical to a fragment of the polynucleotide to be detected, because using such a probe gives 100% success in detecting said DNA molecule.

Thus, the claimed invention was within the ordinary skill in the art to make and use at the time it was made and was as a whole, *prima facie* obvious.

Claims 14-22 are rejected under 35 U.S.C. 103(a) as being unpatentable over Adams et al. homo sapiens cDNA sequence AA311750 (Initial assessment of human gene diversity and expression patterns based on 83 million nucleotides of cDNA sequence, Nature 377 (6547 Suppl), 3-174, 1995) in the view of common knowledge in the field of molecular biology.

The claims are directed to a method of detecting a nucleic acid in a sample, comprising:

a) combining the sample with a polynucleotide primer such that the primer initiates amplification of nucleic acid encoding at least a fragment of hTRT if presenting the sample; and

b) detecting any amplified product formed as result of a) wherein the polynucleotide primer comprises a sequence identical or complementary to at least 15 consecutive nucleotides contained in SEQ ID NO: 224.

Adams and al. teach Homo sapiens cDNA 5' sequence identified as locus AA311750. This EST sequence is 258 nucleotides long, and exhibits 97.7% homology with the fragment of SEQ ID NO: 224 which consists of nucleotides 2649-2906. AA311750 comprises 164 nucleotide long, 20 nucleotide long, and 64 nucleotide long consecutive fragments of SEQ ID NO: 224; see sequence alignment.

Adams et al. do not teach the use of 164, 64 and 20 nucleotide long fragments as primers in detecting a nucleic acid in the sample by amplification. However, one skilled in the art knows that EST sequences are created to be used for detecting a presence of the sequences that are homologous to them.

It would have been obvious to one having ordinary skill in the art at the time of invention to use for detecting of a DNA the fragments of AA311750 sequence. The motivation is to use as primers DNA molecules that are 100% identical to SEQ ID NO: 224 because using such primers gives 100% success in amplifying hTRT DNA molecule.

Thus, the claimed invention was within the ordinary skill in the art to make and use at the time it was made and was as a whole, *prima facie* obvious.

In addition, claims 14-20 are rejected rejected under 35 U.S.C. 103(a) as being unpatentable over Straussberg who discloses *Homo sapiens* cDNA sequence AA281296, see the encloses NCBI Sequence Viewer printout. As indicted in the enclosed sequence alignment, the sequence covers nucleotides 1679-2067 of SEQ ID NO:224. The sequence was entered to NBCI data base in April 1997.

4. Conclusion

All claims are rejected.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Malgorzata A. Walicka, Ph.D., whose telephone number is (703) 305-7270. The examiner can normally be reached Monday-Friday from 10:00 a.m. to 4:30 p.m.

If attempts to reach examiner by telephone are unsuccessful, the examiner's supervisor, Ponnathapura Achutamurthy, Ph.D. can be reached on (703) 308-3804. The fax phone number for this Group is (703) 305-3014.

Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionists whose telephone number is (703) 308-0196.

Malgorzata A. Walicka, Ph.D.

Patent Examiner

Art Unit 1652

PONNATHAPU ACHUTAMURTHY
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600